Output tables for 1xN statistical comparisons.

December 17, 2022

1 Average rankings of Friedman Alligned test

Average ranks obtained by each method in the Friedman Alligned test.

Algorithm	Ranking
MEABC	165.0172
ABCADE	80.2931
ABCNG	132.7069
SHADE	74.3276
MAPSO	75.7931
TAPSO	124.0862
MEEABC	61.7759

Table 1: Average Rankings of the algorithms (Aligned Friedman)

Aligned Friedman statistic (distributed according to chi-square with 6 degrees of freedom): 24.513275.
P-value computed by Aligned Friedman Test: 0.000420059612.

2 Post hoc comparison (Friedman Alligned)

P-values obtained in by applying post hoc methods over the results of Friedman Alligned procedure.

i	algorithm	$z = (R_0 - R_i)/SE$	p	Holm	Hochberg	Hommel	Holland	Rom
6	MEABC	6.692145	0	0.008333			0.008512	0.008764
5	ABCNG	4.597776	0.000004	0.01			0.010206	0.010515
4	TAPSO	4.03898	0.000054	0.0125			0.012741	0.013109
3	ABCADE	1.200294	0.230025	0.016667			0.016952	0.016667
2	MAPSO	0.908603	0.36356	0.025			0.025321	0.025
1	SHADE	0.813607	0.41587	0.05			0.05	0.05

Table 2: Post Hoc comparison Table for $\alpha = 0.05$ (FRIEDMAN ALLIGNED)

Bonferroni-Dunn's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.008333.
Holm's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.016667.
Hochberg's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.0125.
Hommel's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.016667.
Holland's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.016952.
Rom's procedure rejects those hypotheses that have an unadjusted p-value ≤ 0.013109.

3 Adjusted P-Values (Friedman Alligned)

Adjusted P-values obtained through the application of the post hoc methods (Friedman Alligned).

i	algorithm	unadjusted p	p_{Bonf}	p_{Holm}	$p_{Hochberg}$	p_{Hommel}
1	MEABC	0	0	0	0	0
2	ABCNG	0.000004	0.000026	0.000021	0.000021	0.000021
3	TAPSO	0.000054	0.000322	0.000215	0.000215	0.000215
4	ABCADE	0.230025	1.38015	0.690075	0.41587	0.41587
5	MAPSO	0.36356	2.181359	0.72712	0.41587	0.41587
6	SHADE	0.41587	2.495219	0.72712	0.41587	0.41587

Table 3: Adjusted p-values (ALIGNED FRIEDMAN) (I)

i	algorithm	unadjusted p	$p_{Holland}$	p_{Rom}
1	MEABC	0	0	0
2	ABCNG	0.000004	0.000021	0.00002
3	TAPSO	0.000054	0.000215	0.000205
4	ABCADE	0.230025	0.543511	0.41587
5	MAPSO	0.36356	0.594944	0.41587
6	SHADE	0.41587	0.594944	0.41587

Table 4: Adjusted p-values (ALIGNED FRIEDMAN) (II)